



UNITED STATES PATENT AND TRADEMARK OFFICE

EST

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/664,859	09/22/2003	Konrad Basler	Q-77377	4459

7590 11/23/2005

SUGHRUE MION, PLLC
2100 Pennsylvania Avenue, NW
Washington, DC 20037-3213

EXAMINER

CARLSON, KAREN C

ART UNIT	PAPER NUMBER
----------	--------------

1653

DATE MAILED: 11/23/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No. 10/664,859	Applicant(s) BASLER ET AL	
	Examiner Karen Cochran Carlson, Ph.D.	Art Unit 1653	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☐ Responsive to communication(s) filed on ____.
- 2a) ☐ This action is FINAL. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 61-66 is/are pending in the application.
- 4a) Of the above claim(s) ____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) ____ is/are allowed.
- 6) ☒ Claim(s) 61-66 is/are rejected.
- 7) ☐ Claim(s) ____ is/are objected to.
- 8) ☐ Claim(s) ____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on ____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. ____.
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- | | |
|--|--|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892) | 4) <input type="checkbox"/> Interview Summary (PTO-413)
Paper No(s)/Mail Date. ____ |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | 5) <input type="checkbox"/> Notice of Informal Patent Application (PTO-152) |
| 3) <input checked="" type="checkbox"/> Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date <u>9/22/03</u> . | 6) <input checked="" type="checkbox"/> Other: <u>3 SEQ attachments</u> . |

Art Unit: 1653

Claims 1-60 have been cancelled. New Claims 61-66 are currently pending and are under examination.

Priority is set to July 28, 2000.

Sequence Compliance:

There is no amino acid sequence identifier depicting the amino acid sequence depicted in Figure 2, or under the nucleotide sequence of SEQ ID NO: 1. Thus, the Sequence Rules have not been met.

Further, upon finding the art of Venter et al. (US PG Pub 2005/0208558), the search of polypeptides encoded by the nucleotide sequence of SEQ ID NO: 1 shows that Venter et al.'s SEQ ID NO: 3129 is identical to residues 6-1429 of this amino acid sequence, herein now to be referred to as SEQ ID NO: X to help prevent confusion of what is instant SEQ ID NO: 1 (a nucleotide sequence) versus what Applicants claim SEQ ID NO: 1 to be (both nucleotide and amino acid sequences). However, perusal of the C-terminal amino acids of SEQ ID NO: X shows that these amino acids correspond to the C-terminal of Venter et al.'s SEQ ID NO: 3129, that is, the string of amino acids N-terminal of residue 1464 is the same as Venter et al.'s string of amino acids N-terminal to residue 1429. Thus, there is a discrepancy of 40 amino acids (5 at the N-terminus of SEQ ID NO: 3129 and 40 somewhere in-between the N- and C-terminal of SEQ ID NO: X).

Venter et al.'s SEQ ID NO: 3129 is 1429 amino acid in length, of which amino acids 6-1429 are identical to the computer readable form of instant SEQ ID NO: X as determined by the Examiner's perusal of the sequence search. However, SEQ ID NO: X is 1464 amino acids long in paper form. Upon perusal of Venter et al.'s SEQ ID NO: 3129 and SEQ ID NO: X of the instant paper copy of the Sequence listing, amino acids 1140-1179 of the paper form of SEQ ID NO: X is

Art Unit: 1653

missing in SEQ ID NO: 3129 at amino acid position 1144-1145 of SEQ ID NO: 3129. When the sequence search was reviewed again, the nucleotides encoding these same amino acids (nucleotides 5482-5601 of SEQ ID NO: 1) are missing from the computer readable form of instant SEQ ID NO: 1. Thus, the paper copy and the computer readable form of SEQ ID NO: 1 are not identical.

Thus:

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth above.

Applicants must comply with the sequence rules in response to this office or their response will be held non-responsive.

The disclosure is objected to because of the following informalities:

At page 1, para. 2, line 1, "cystein" should be written as --- cysteine ---.

At page 18 and 39, the sequence identifiers are not placed after the sequences.

At page 32, para. 2, line 4, "Cels" should be written as --- cells ---.

At page 10+, the figure legends must refer to "Figure 1(A), Figure 1(B), and so on, for example, because there is no figure "B" or "Figure 1" in the drawings. See also the legends for figures 3, 5, 7, 8, 10, 11, 12, 13, and 15.

Also, reference to the figures throughout the specification must refer to the specifically named figure. That is, at page 22, para. 3, Figure 1 is referred to instead of "Figure 1(A), for example. See also reference to Figure 7 at page 24, para. 2 and page 26, line 4; Figure 8 at page 27, line 8; and Figures 8 and 10 at page 30, para. 1, for example.

Art Unit: 1653

It is noted that parent application 09/915,543 has been allowed. Upon issuance of this application the priority information at page 1 of the specification will have to be updated.

Appropriate correction is required.

The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See MPEP § 608.01.

Hyperlinks can be found at pages 23, 29, and 41. Applicants should delete http:// to remove the hyperlink.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 61-66 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claims 61 and 62 refer to nucleotide sequence SEQ ID NO: 1 as both the nucleic acid encoding and the amino acid sequence depicting dlgs. Thus, it is not clear what sequence identifies the amino acid sequence. Additionally, Claim 61 refers to amino acids 1-1464 of SEQ ID NO: 1, while the computer readable form of the translation of SEQ ID NO: 1 depicts an amino acid sequence of 1429 amino acids (ie, SEQ ID NO: X).

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make

Art Unit: 1653

and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 61-66 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claim 65 refers to chimeric polypeptides comprising dlgs (variants and fragments) and glutathione-S-transferase, thioredoxin, or an antibody. At page 6, para. 2 of the specification, the specification states that chimeric polypeptide will comprise dlgs (variants and fragments) and an epitope sequence tag, glutathione-S-transferase, beta-galactosidase, or alkaline phosphatase. Claim 65 is a new claim and is not part of the original disclosure. Thus, the inclusion of thioredoxin, or an antibody as being part of a chimeric polypeptide with dlgs (variants and fragments) is new matter.

Regarding written description, the specification does not describe variants of SEQ ID NO: X having at least 90% identity to SEQ ID NO: X, or biologically active fragments of SEQ ID NO: X. While the claims state that the fragments of SEQ ID NO: X will bind to an antibody against itself, this is not a biological activity, but rather a circular activity, that is, there is no reason for one of skill in the art to use an antibody to bind a fragment of SEQ ID NO: 1 if that fragment has no known activity.

Regarding the written description for dlgs fragments SEQ ID NO: 2, 4, 6, 8, or 10, SEQ ID NO: 2 has been shown to bind Doll (page 37). However, the specification fails to address any activity associated with SEQ ID NO: 4, 6, 8, or 10. Thus, without a correlation of structure to function, these sequences lack written description.

Art Unit: 1653

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(e) the invention was described in a patent granted on an application for patent by another filed in the United States before the invention thereof by the applicant for patent, or on an international application by another who has fulfilled the requirements of paragraphs (1), (2), and (4) of section 371(c) of this title before the invention thereof by the applicant for patent.

Claims 61, 62, 63, and 66 are rejected under 35 U.S.C. 102(e) as being anticipated by Venter et al. (Pub. No. US 2005/0208558). Venter et al.'s SEQ ID NO: 3129 is the same as SEQ ID NO: 3135 in Venter et al.'s provisional application 60/191,637, filed March 23, 2000.

Venter et al. teach SEQ ID NO: 3129, which encompasses amino acids 6-1429 of SEQ ID NO: X as shown in the sequence search (back translation of the computer readable form of SEQ ID NO: 1). Thus, for the purposes of this rejection in view of the noncompliance of the Sequence Rules as noted above, Venter et al. anticipate SEQ ID NO: X (Claims 61, 62), polypeptides having at least 90% identity to SEQ ID NO: X (Claim 61), and polypeptides comprising fragments of SEQ ID NO: X (Claim 61).

Even if the paper form of SEQ ID NO: X were used, the sequences would share 97.2% sequence identity (1423/1464; Claim 61).

Regarding fragments, SEQ ID N: 2, 4, 6, 8, and 10 can be found at amino acid positions 323-334, 520-554, 711-725, 760-768, and 773-884, respectively, in Venter et al.'s SEQ ID NO: 3129 (Claim 63).

At para.[0016] of Venter et al., these polypeptides are placed in pharmaceutical compositions (Claim 66).

No Claims are allowed.

Art Unit: 1653

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Karen Cochrane Carlson, Ph.D. whose telephone number is 571-272-0946.

The examiner can normally be reached on 7:00 AM - 4:00 PM, off alternate Fridays.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Dr. Jon Weber can be reached on 571-272-0925. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

A handwritten signature in black ink that reads "Karen Cochrane Carlson" followed by a stylized monogram or initials.

**KAREN COCHRANE CARLSON, PH.D
PRIMARY EXAMINER**

10/664 859

Attach #1

Marked up
Seq ID NO: 1
"MO: X"

SEQUENCE LISTING

<110> BASLER, Konrad
BRUNNER, Erich
FROESCH, Barbara
KRAMPS, Thomas
PETER, Oliver

<120> ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATHWAY AND THERAPEUTIC
AND DIAGNOSTIC APPLICATIONS BASED THEREON

<130> Q60361

<140> 09/915,543

<141> 2001-07-27

<150> 60/221,502

<151> 2000-07-28

<160> 22

<170> PatentIn version 3.1

<210> 1

<211> 6909

<212> DNA

<213> Drosophila lgs

<220>

<221> exon

<222> (691)..(981)

<223>

<220>

<221> exon

<222> (468)..(632)

<223>

<220>

<221> exon

<222> (1456)..(1665)

<223>

<220>

<221> exon

<222> (2394)..(4397)

<223>

<220>

<221> exon

<222> (4679)..(4870)

<223>

<223>

1

5

10

15

20

25

30

35

40

45

50

55

55

60

65
61

70

75

80

85

90

95

100

105

110

tcc agt gaa cac tcg aat agc agc aat gtg tct gct aca gtg ggc ctt	915
Ser Ser Glu His Ser Asn Ser Ser Asn Val Ser Ala Thr Val Gly Leu	
115 120 125 130	
act cag atg gta gat tgt gac gag caa tcg aag aaa aac aaa tgt agt	963
Thr Gln Met Val Asp Cys Asp Glu Gln Ser Lys Lys Asn Lys Cys Ser	
135 140 145	
gtg aag gac gag gaa gct ggtaagactg ccctacaaat ggtttaaaat	1011
Val Lys Asp Glu Glu Ala	
150	
tttaaaatgt attggcggttc acctttgtta atcatttaat tgtttttttt ttgctatact	1071
tacaatttta gttttaaaact tgtaaacttg actaaaactc gcgaagctcg gatcaaaaca	1131
gacattttct tggaaccgta attaagctca taaaaatatt aattcatctt gatggaatgc	1191
atatcataga tgtactcaaa catctcaaga aagacctcaa attggatcaa ctaattagtt	1251
tgagaaaaaa ttgctgtact tttagaata tattaattta aaaatttgct gagtgaaatg	1311
atataatagt cacaataatt tttagttaaa ctgctaaagc attttgaata gccgtgctac	1371
gcagatgcta ctagacgcgg tgtaaaagct aattttttatt taaaagctgt cctaatatcc	1431
cataaccatt aatgtcccat ttca gaa ata agt tct aat aaa gca aaa ggt	1482
Glu Ile Ser Ser Asn Lys Ala Lys Gly	
155 160	
caa gca gct ggt ggc ggc tgc gaa aca ggt tct aca tcc agt ttg act	1530
Gln Ala Ala Gly Gly Gly Cys Glu Thr Gly Ser Thr Ser Ser Leu Thr	
165 170 175	
gtc aag gaa gaa ccc acc gat gtc tta ggc agt tta gta aat atg aaa	1578
Val Lys Glu Glu Pro Thr Asp Val Leu Gly Ser Leu Val Asn Met Lys	
180 185 190	
aaa gaa gaa aga gaa aat cat tcg cca acg atg tcc cct gtt ggt ttt	1626
Lys Glu Glu Arg Glu Asn His Ser Pro Thr Met Ser Pro Val Gly Phe	
195 200 205	
ggc tca att ggt aat gca cag gac aac tcc gct aca ccg ggtaagtttt	1675
Gly Ser Ile Gly Asn Ala Gln Asp Asn Ser Ala Thr Pro	
210 215 220	
aagagatcca tataaagcaa ataacaagaa ttaatgtcag ttaccaattt tatttgatag	1735
tcaaagaact actatagcga tatctcctgc cttttaattt tattttaatt aggaaatagc	1795
aatatttcta atttgtaaaa taaaattgat taattaacta gaatttaaaa accttttgaa	1855
ttaggacata cccttccaaa aatcagtaat cattgggaac gagagtgtgg tcccgaagga	1915
gactactata aaaccttttg agctatctga tactgcacgc tactaaaaat gattagttta	1975

ggaaaatggg tgtaattttg taggaagttt tcattttaga agaaatgtga ttattttatt	2035
aaaccccttc aagcggaact acatttggtc tacgatattt tggaaaaaca aatggttaag	2095
ttggaaagtg cctataaaac agaattccac ggtttcaaact actaaccagg tttttgattt	2155
aattttgatt aaatgagaaa ttatcacact tcagttaaaa tgtttaattc gattaaggtc	2215
ggacaatcac agcagatttc catttttgcg tgtatatata gaagtcgcct tcacactctt	2275
ctggcgcgct tcaccactac gtggagttcc gccgcagtg atttatatag atgatttacg	2335
agttatttaa ttttttatgg tgtattttaa taaatatctt atttattcat tttacata	2393
gtt aaa att gaa aga att tca aac gac agt acc acg gaa aaa aaa gga Val Lys Ile Glu Arg Ile Ser Asn Asp Ser Thr Thr Glu Lys Lys Gly 225 230 235	2441
tcg tcc ttg aca atg aat aat gac gaa atg agc atg gaa ggc tgc aat Ser Ser Leu Thr Met Asn Asn Asp Glu Met Ser Met Glu Gly Cys Asn 240 245 250	2489
cag ttg aat ccc gat ttt atc aat gaa tct tta aat aat cct gca att Gln Leu Asn Pro Asp Phe Ile Asn Glu Ser Leu Asn Asn Pro Ala Ile 255 260 265 270	2537
tcg agc ata tta gta agc gga gta gga cca ata ccc gga atc gga gtt Ser Ser Ile Leu Val Ser Gly Val Gly Pro Ile Pro Gly Ile Gly Val 275 280 285	2585
gga gcg ggg acg gga aat tta ttg act gcc aac gcc aat gga atc tcc Gly Ala Gly Thr Gly Asn Leu Leu Thr Ala Asn Ala Asn Gly Ile Ser 290 295 300	2633
tcg ggt agc agt aat tgt ttg gat tac atg caa cag caa aat cac ata Ser Gly Ser Ser Asn Cys Leu Asp Tyr Met Gln Gln Gln Asn His Ile 305 310 315	2681
ttc gtg ttt tca act cag ctg gcc aac aaa ggg gcc gaa tca gtt tta Phe Val Phe Ser Thr Gln Leu Ala Asn Lys Gly Ala Glu Ser Val Leu 320 325 330	2729
agc ggt caa ttt caa act att att gcg tat cac tgc act cag cct gct Ser Gly Gln Phe Gln Thr Ile Ile Ala Tyr His Cys Thr Gln Pro Ala 335 340 345 350	2777
aca aaa agc ttc ctg gaa gac ttt ttt atg aaa aac cct tta aag att Thr Lys Ser Phe Leu Glu Asp Phe Phe Met Lys Asn Pro Leu Lys Ile 355 360 365	2825
aac aag tta cag cgg cac aat tcc gtc ggt atg cca tgg ata ggc atg Asn Lys Leu Gln Arg His Asn Ser Val Gly Met Pro Trp Ile Gly Met 370 375 380	2873
ggg cag gtt gga cta act cct cct aat cct gta gcc aaa ata aca caa Gly Gln Val Gly Leu Thr Pro Pro Asn Pro Val Ala Lys Ile Thr Gln 385 390 395	2921

NO.2

cag cag cca cat aca aag acc gta ggc cta ttg aaa ccc caa ttc aat	2969
Gln Gln Pro His Thr Lys Thr Val Gly Leu Leu Lys Pro Gln Phe Asn	
400 405 410	
caa cat gaa aac agc aaa cgt agt act gta agc gcg cct agc aac tct	3017
Gln His Glu Asn Ser Lys Arg Ser Thr Val Ser Ala Pro Ser Asn Ser	
415 420 425 430	
ttt gtc gac cag tct gat cct atg ggc aac gaa act gaa ttg atg tgc	3065
Phe Val Asp Gln Ser Asp Pro Met Gly Asn Glu Thr Glu Leu Met Cys	
435 440 445	
tgg gaa ggc gga tcc tca aac acc agt agg tct gga caa aac tca cga	3113
Trp Glu Gly Gly Ser Ser Asn Thr Ser Arg Ser Gly Gln Asn Ser Arg	
450 455 460	
aat cat gta gac agt atc agt aca tcc agc gag tca cag gca ata aag	3161
Asn His Val Asp Ser Ile Ser Thr Ser Ser Glu Ser Gln Ala Ile Lys	
465 470 475	
ata ctg gaa gca gct ggc gtt gat ttg gga cag gtc aca aaa gga agc	3209
Ile Leu Glu Ala Ala Gly Val Asp Leu Gly Gln Val Thr Lys Gly Ser	
480 485 490	
gat cct ggc ctg aca act gaa aac aac att gta tca ctg caa gga gtt	3257
Asp Pro Gly Leu Thr Thr Glu Asn Asn Ile Val Ser Leu Gln Gly Val	
495 500 505 510	
aag gtt cca gac gaa aac ctt aca cca caa cag cgg caa cat cgg gaa	3305
Lys Val Pro Asp Glu Asn Leu Thr Pro Gln Gln Arg Gln His Arg Glu	
515 520 525	
gaa cag ttg gca aaa ata aaa aaa atg aat caa ttt ctt ttt cct gaa	3353
Glu Gln Leu Ala Lys Ile Lys Lys Met Asn Gln Phe Leu Phe Pro Glu	
530 535 540	
aat gag aat tca gta gga gct aat gta agc tca cag ata aca aaa att	3401
Asn Glu Asn Ser Val Gly Ala Asn Val Ser Ser Gln Ile Thr Lys Ile	
545 550 555	
cca gga gat tta atg atg ggg atg tcg ggt ggc gga ggc gga tct att	3449
Pro Gly Asp Leu Met Met Gly Met Ser Gly Gly Gly Gly Gly Ser Ile	
560 565 570	
ata aat ccg acg atg cga caa ctg cat atg cca ggt aac gcc aaa tcg	3497
Ile Asn Pro Thr Met Arg Gln Leu His Met Pro Gly Asn Ala Lys Ser	
575 580 585 590	
gag ctc tta tcg gcg aca agt tca gga ctt tcg gaa gat gta atg cat	3545
Glu Leu Leu Ser Ala Thr Ser Ser Gly Leu Ser Glu Asp Val Met His	
595 600 605	
cca ggg gat gtt ata tca gat atg ggt gcc gta ata gga tgt aat aat	3593
Pro Gly Asp Val Ile Ser Asp Met Gly Ala Val Ile Gly Cys Asn Asn	
610 615 620	

aat caa aaa acc agt gtg caa tgt gga tct gga gta ggt gtt gtc act Asn Gln Lys Thr Ser Val Gln Cys Gly Ser Gly Val Gly Val Val Thr 625 630 635	3641
gga aca act gca gct gga gta aat gtc aat atg cat tgc tca agc tcc Gly Thr Thr Ala Ala Gly Val Asn Val Asn Met His Cys Ser Ser Ser 640 645 650	3689
ggc gcc ccg aat ggc aat atg atg gga agc tct acg gat atg cta gcc Gly Ala Pro Asn Gly Asn Met Met Gly Ser Ser Thr Asp Met Leu Ala 655 660 665 670	3737
tcg ttt ggc aac aca agc tgc aac gtc atc gga acg gcc cca gat atg Ser Phe Gly Asn Thr Ser Cys Asn Val Ile Gly Thr Ala Pro Asp Met 675 680 685	3785
tct aag gaa gtt tta aat caa gat agc cga acc cat tca cat caa ggg Ser Lys Glu Val Leu Asn Gln Asp Ser Arg Thr His Ser His Gln Gly 690 695 700	3833
gga gtt gct caa atg gag tgg tcg aag att caa cat caa ttt ttc gaa Gly Val Ala Gln Met Glu Trp Ser Lys Ile Gln His Gln Phe Phe Glu 705 710 715	3881
gaa cgc ctc aag ggg ggc aag ccc aga caa gtc act gga act gta gta Glu Arg Leu Lys Gly Gly Lys Pro Arg Gln Val Thr Gly Thr Val Val 720 725 730	3929
cca caa cag caa acc cct tct gga tct ggt gga aac tcg tta aac aac Pro Gln Gln Gln Thr Pro Ser Gly Ser Gly Gly Asn Ser Leu Asn Asn 735 740 745 750	3977
cag gtg cga ccc ctg caa ggt cca cct cct cct tac cac tcc atc cag Gln Val Arg Pro Leu Gln Gly Pro Pro Pro Pro Tyr His Ser Ile Gln 755 760 765	4025
aga tct gcg tca gta cca ata gcc act caa tcg ccc aat ccc tcg agt Arg Ser Ala Ser Val Pro Ile Ala Thr Gln Ser Pro Asn Pro Ser Ser 770 775 780	4073
cca aac aat cta tct ctc ccg tca ccg cgg aca acc gca gca gtc atg Pro Asn Asn Leu Ser Leu Pro Ser Pro Arg Thr Thr Ala Ala Val Met 785 790 795	4121
gga ttg ccg acc aac tct cct agc atg gat gga aca gga tca tta tct Gly Leu Pro Thr Asn Ser Pro Ser Met Asp Gly Thr Gly Ser Leu Ser 800 805 810	4169
gga tct gtt ccg caa gct aat act tcg acg gtt cag gca ggc aca aca Gly Ser Val Pro Gln Ala Asn Thr Ser Thr Val Gln Ala Gly Thr Thr 815 820 825 830	4217
aca gtg ctc tca gca aac aag aac tgt ttt cag gca gac acc cca tcg Thr Val Leu Ser Ala Asn Lys Asn Cys Phe Gln Ala Asp Thr Pro Ser 835 840 845	4265
ccg tca aat caa aat cgt agt aga aat acc gga tcg tca agc gtt ctt	4313

Pro Ser Asn Gln Asn Arg Ser Arg Asn Thr Gly Ser Ser Ser Val Leu	
850 855 860	
acg cat aac tta agc agc aac cca agt acc ccc tta tct cat cta tcc	4361
Thr His Asn Leu Ser Ser Asn Pro Ser Thr Pro Leu Ser His Leu Ser	
865 870 875	
cca aag gaa ttt gag tct ttc ggt cag tcc tct gct ggtatggtat	4407
Pro Lys Glu Phe Glu Ser Phe Gly Gln Ser Ser Ala	
880 885 890	
atttggttttaa ttttttttaaa gacaaatcaa atatgaattg cgtaaataat aagttatata	4467
ttacataact cggaaatttg atagaaaaaa tcaggaatag aaaaaataaa ttatttttccg	4527
gaccgcccac ccatttcttg aatccaattt ctggagtgat tgtagagat aatctactat	4587
taaaattaaa cacgaaaatt catatccggt aattgaaaat cactattggt taataagaaa	4647
ttaaaaatat gtttattata atattttctac a ggt gat aac atg aaa agt agg	4699
Gly Asp Asn Met Lys Ser Arg	
895	
cga cca agc cca cag ggt cag cgg tca cca gta aat agt cta ata gag	4747
Arg Pro Ser Pro Gln Gly Gln Arg Ser Pro Val Asn Ser Leu Ile Glu	
900 905 910	
gca aat aaa gat gta cga ttt gct gca tcc agt cct ggt ttt aac ccg	4795
Ala Asn Lys Asp Val Arg Phe Ala Ala Ser Ser Pro Gly Phe Asn Pro	
915 920 925	
cat cca cat atg caa agc aat tca aat tca gca tta aac gcc tat aaa	4843
His Pro His Met Gln Ser Asn Ser Asn Ser Ala Leu Asn Ala Tyr Lys	
930 935 940 945	
atg ggc tct acc aat ata cag atg gag gtaaataattt aaatatttta	4890
Met Gly Ser Thr Asn Ile Gln Met Glu	
950	
tttaacgttt ttgtgtaaat ttatcttctt tttcag cgt caa gca tca gcg caa	4944
Arg Gln Ala Ser Ala Gln	
955 960	
ggt gga tcc gta caa ttt agt cgg cgc tcc gat aat att ccg cta aat	4992
Gly Gly Ser Val Gln Phe Ser Arg Arg Ser Asp Asn Ile Pro Leu Asn	
965 970 975	
ccc aat agt ggc aat cgg ccg cca cca aac aag atg acc caa aac ttc	5040
Pro Asn Ser Gly Asn Arg Pro Pro Pro Asn Lys Met Thr Gln Asn Phe	
980 985 990	
gat cca atc tct tct ttg gca caa atg tcc caa caa cta aca agt tgc	5088
Asp Pro Ile Ser Ser Leu Ala Gln Met Ser Gln Gln Leu Thr Ser Cys	
995 1000 1005	
gtg tcc agc atg ggt agt cca gcc gga act ggt ggt atg acg atg	5133
Val Ser Ser Met Gly Ser Pro Ala Gly Thr Gly Gly Met Thr Met	

1010	1015	1020	
atg ggg ggt ccg gga ccg tcc Met Gly Gly Pro Gly Pro Ser 1025	gac atc aat att gag Asp Ile Asn Ile Glu 1030	cat gga ata His Gly Ile 1035	5178
att tcg gga cta gat gga tca Ile Ser Gly Leu Asp Gly Ser 1040	gga ata gat acc ata Gly Ile Asp Thr Ile 1045	aat caa aat Asn Gln Asn 1050	5223
aac tgt cat tca atg aat gtc Asn Cys His Ser Met Asn Val 1055	gta atg aac tca atg Val Met Asn Ser Met 1060	ggg ccc cga Gly Pro Arg 1065	5268
atg ctg aat cct aaa atg tgc Met Leu Asn Pro Lys Met Cys 1070	gta gca ggc ggt cca Val Ala Gly Gly Pro 1075	aat gga ccg Asn Gly Pro 1080	5313
cct ggc ttt aat cct aat tcc Pro Gly Phe Asn Pro Asn Ser 1085	ccc aat ggt gga tta Pro Asn Gly Gly Leu 1090	aga gag aat Arg Glu Asn 1095	5358
tcc ata ggg tct ggc tgt ggc Ser Ile Gly Ser Gly Cys Gly 1100	tca gca aac tct tca Ser Ala Asn Ser Ser 1105	aac ttt caa Asn Phe Gln 1110	5403
ggg gtt gtt cca cct ggt gcc Gly Val Val Pro Pro Gly Ala 1115	aga atg atg ggt cga Arg Met Met Gly Arg 1120	atg cca gtc Met Pro Val 1125	5448
aat ttt ggt tcg aat ttc aat Asn Phe Gly Ser Asn Phe Asn 1130	ccg aat att cag gta Pro Asn Ile Gln Val 1135	aag gcg agt Lys Ala Ser 1140	5493
acc cca aac acc ata caa tac Thr Pro Asn Thr Ile Gln Tyr 1145	atg cca gta agg gca Met Pro Val Arg Ala 1150	cag aac gcc Gln Asn Ala 1155	5538
aac aac aat aac aac aat gga Asn Asn Asn Asn Asn Asn Gly 1160	gct aat aat gtg cga Ala Asn Asn Val Arg 1165	atg cca cct Met Pro Pro 1170	5583
agt ctg gaa ttt ttg cag Ser Leu Glu Phe Leu Gln 1175	agg tac gct aac cct caa Arg Tyr Ala Asn Pro Gln 1180	atg ggt gct Met Gly Ala 1185	5628
gta ggc aat ggg tcg cca ata Val Gly Asn Gly Ser Pro Ile 1190	tgc cca cca tca gcc Cys Pro Pro Ser Ala 1195	agc gac ggt Ser Asp Gly 1200	5673
act cct gga atg cca gga ttg Thr Pro Gly Met Pro Gly Leu 1205	atg gcg gga cca gga Met Ala Gly Pro Gly 1210	gcc gga ggt Ala Gly Gly 1215	5718
atg cta atg aat tct tcc gga Met Leu Met Asn Ser Ser Gly 1220	gag caa cac cag aac Glu Gln His Gln Asn 1225	aag atc aca Lys Ile Thr 1230	5763

5482 not in Ventner

40aa

5601

aac aat cct ggg gca agc aat ggt att aac ttc ttt cag aat tgc	5808
Asn Asn Pro Gly Ala Ser Asn Gly Ile Asn Phe Phe Gln Asn Cys	
1235 1240 1245	
aat caa atg tct att gtt gac gaa gag ggt gga tta ccc ggc cat	5853
Asn Gln Met Ser Ile Val Asp Glu Glu Gly Gly Leu Pro Gly His	
1250 1255 1260	
gac gga tca atg aat att ggt caa cca tct atg ata agg ggc atg	5898
Asp Gly Ser Met Asn Ile Gly Gln Pro Ser Met Ile Arg Gly Met	
1265 1270 1275	
cgt cca cat gcc atg cgg cca aat gta atg ggt gcg cgg atg cca	5943
Arg Pro His Ala Met Arg Pro Asn Val Met Gly Ala Arg Met Pro	
1280 1285 1290	
ccc gtt aac agg caa att cag ttt gca cag tca tcg gat ggt att	5988
Pro Val Asn Arg Gln Ile Gln Phe Ala Gln Ser Ser Asp Gly Ile	
1295 1300 1305	
gac tgt gtc ggg gat ccg tca tca ttt ttc act aac gct tcc tgc	6033
Asp Cys Val Gly Asp Pro Ser Ser Phe Phe Thr Asn Ala Ser Cys	
1310 1315 1320	
aac agc gct gga cca cac atg ttt gga tca gca caa cag gcc aat	6078
Asn Ser Ala Gly Pro His Met Phe Gly Ser Ala Gln Gln Ala Asn	
1325 1330 1335	
cag cct aag aca caa cac ata aag aac ata cct agt gga atg tgt	6123
Gln Pro Lys Thr Gln His Ile Lys Asn Ile Pro Ser Gly Met Cys	
1340 1345 1350	
caa aac caa tcg gga ctt gca gtg gca caa ggg cag atc caa ctg	6168
Gln Asn Gln Ser Gly Leu Ala Val Ala Gln Gly Gln Ile Gln Leu	
1355 1360 1365	
cat ggg caa gga cat gcg cag ggt cag tct tta att gga cct act	6213
His Gly Gln Gly His Ala Gln Gly Gln Ser Leu Ile Gly Pro Thr	
1370 1375 1380	
aat aat aat tta atg tca act gcc gga agt gtc agt gct act aac	6258
Asn Asn Asn Leu Met Ser Thr Ala Gly Ser Val Ser Ala Thr Asn	
1385 1390 1395	
ggg gtc tct ggc atc aat ttc gta ggt ccc tct tct acg gac ctg	6303
Gly Val Ser Gly Ile Asn Phe Val Gly Pro Ser Ser Thr Asp Leu	
1400 1405 1410	
aag tat gcc cag caa tat cat agt ttt cag cag cag tta tat gct	6348
Lys Tyr Ala Gln Gln Tyr His Ser Phe Gln Gln Gln Leu Tyr Ala	
1415 1420 1425	
acc aac acc aga agt caa caa caa cag cat atg cac cag cag cac	6393
Thr Asn Thr Arg Ser Gln Gln Gln Gln His Met His Gln Gln His	
1430 1435 1440	

cag agc	aac atg	ata aca	atg ccg	ccg aat	tta tca	cca aat	cca		6438
Gln Ser	Asn Met	Ile Thr	Met Pro	Pro Asn	Leu Ser	Pro Asn	Pro		
1445			1450			1455			

acg ttc	ttt gtc	aac aaa	taaacttcta	aatttttgcc	gccctcgtca		6486
Thr Phe	Phe Val	Asn Lys					
1460							

tgtattgttt	actagtctcc	aaattaagac	atgcatctct	aaataagatt	ttttgaagct		6546
tatttactta	ggtgttttta	caacggagaa	aataaacttt	tggatatgca	aatgataacg		6606
ttggaaacaa	cataattcat	ttgcaacttt	tagaagtcac	gtcgaagtta	aatgtagaat		6666
ctgtatttta	acataatagg	tcattctgtaa	aaataattaa	acatcgaaat	tttagttatc		6726
agcagctatt	ttctgttatt	atttaatatg	tgcgctgctc	tctctgtgtt	aatgaaatt		6786
aaaatatata	tataaatgta	aaacgctatt	gatatatatt	gctctcaact	gtattgtaat		6846
caatattaag	agaactgtaa	attcttccat	ataaaggtaa	tgaaaaaaaa	aaaaaaaaaa		6906
aaa							6909

<210> 2
 <211> 28
 <212> PRT
 <213> Drosophila lgs

<400> 2

Ile Phe Val	Phe Ser Thr	Gln Leu Ala	Asn Lys Gly	Ala Glu Ser	Val
1	5		10		15

Leu Ser Gly	Gln Phe Gln	Thr Ile Ile	Ala Tyr His
20		25	

<210> 3
 <211> 28
 <212> PRT
 <213> Human lgs/bcl9

<400> 3

Val Tyr Val	Phe Ser Thr	Glu Met Ala	Asn Lys Ala	Ala Glu Ala	Val
1	5		10		15

Leu Lys Gly	Gln Val Glu	Thr Ile Val	Ser Phe His
20		25	

<210> 4
 <211> 35

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: November 2, 2005, 22:10:58 ; Search time 876.5 Seconds
(without alignments)
6590.438 Million cell updates/sec

Title: US-10-664-859-1
Perfect score: 12037
Sequence: 1 acgagtcgtctctcttatat.....aaaaaaaaaaaaaaaa 6909

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1865214 seqs, 418043040 residues
Total number of hits satisfying chosen parameters: 3730428

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p, model -DEV=xlp
-Q=/cgn2_1/USFTO_spool_p/US10664859/runat_02112005_171806_3577/app_query.fasta_1.7047
-DB=Published Applications AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdd -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10664859 @CGN 1 1 982 @runat_02112005_171806_3577
-NCPUL=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7040	58.5	1429	20	US-11-097-143-3129
2	570	4.7	112	9	US-09-915-543-10
3	570	4.7	112	14	US-10-322-579-10
4	570	4.7	112	15	US-10-664-859-10
5	321.5	2.7	1435	15	US-10-276-774-2178
6	314	2.6	1394	15	US-10-381-247B-18
7	314	2.6	1394	16	US-10-723-860-1764
8	314	2.6	1394	18	US-10-756-149-5163
9	312	2.6	1426	9	US-09-915-543-15
10	312	2.6	1426	14	US-10-322-579-15
11	312	2.6	1426	15	US-10-664-859-15
12	312	2.6	1426	16	US-10-408-765A-1958
13	296.5	2.5	1450	15	US-10-381-247B-17
14	296.5	2.5	1494	15	US-10-381-247B-2
15	269.5	2.2	1594	20	US-11-097-143-17856
16	258.5	2.1	1366	20	US-11-097-143-27555
17	258.5	2.1	2151	20	US-11-097-143-7050
18	256.5	2.1	5322	17	US-10-732-923-8729
19	247.5	2.1	2285	18	US-10-773-446-101
20	242.5	2.0	1161	20	US-11-097-143-38793
21	241.5	2.0	1778	20	US-11-097-143-7035
22	241	2.0	2280	20	US-11-097-143-11742
23	240	2.0	2112	20	US-11-097-143-8001
24	233.5	1.9	1243	16	US-10-408-765A-1964
25	233.5	1.9	1441	15	US-10-355-218-2
26	233.5	1.9	1441	18	US-10-503-050A-2
27	233	1.9	2703	20	US-11-097-143-16689
28	233	1.9	3190	17	US-10-732-923-18448
29	230.5	1.9	3275	18	US-10-840-060-90
30	230.5	1.9	3275	20	US-11-097-143-38103
31	230	1.9	3276	17	US-10-732-923-18447
32	229.5	1.9	2005	9	US-09-735-367B-3
33	228.5	1.9	2063	9	US-09-735-367B-2
34	228.5	1.9	2063	18	US-10-973-858-8
35	228.5	1.9	2063	18	US-10-450-763-47506
36	228	1.9	1424	15	US-10-418-027-1
37	228	1.9	1424	16	US-10-473-127-347
38	228	1.9	1424	16	US-10-473-127-350
39	228	1.9	1424	16	US-10-473-127-360
40	223.5	1.9	1522	16	US-10-473-127-355
41	222.5	1.8	1441	14	US-10-170-682-3
42	222.5	1.8	1459	15	US-10-369-493-6418
43	222.5	1.8	1966	16	US-10-408-765A-2217
44	222.5	1.8	2440	15	US-10-341-434-236
45	222.5	1.8	2440	18	US-10-885-977-35

ALIGNMENTS

RESULT 1
US-11-097-143-3129
Sequence 3129, Appl
Publication No. US2005020858A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
FILE REFERENCE: CL000728 US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/457,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769

Alignment #2
538

```

; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3129
; LENGTH: 1429
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-3129

```

Alignment Scores:	0	Length:	1429
Pred. No.:	7040.00	Matches:	1425
Score:	71.0%	Conservative:	1
Percent Similarity:	71.04%	Mismatches:	3
Best Local Similarity:	58.49%	Indels:	577
Query Match:	20	Gaps:	6
DB:			

US-10-664-859-1 (1-6909) x US-11-097-143-3129 (1-1429)

Qy	453	ATGCTCTGCACAACATGCCCCGAGTCCAAACCCMAACAGCCGCAACCAACTCCGAT	512
Db	1	MetLeuSerThrThrMetProArgSerProThrGlnGlnProGlnProAsnSerAsp	20
Qy	513	GCCTCCTCAACAAAGTGCATCTGCATCAAAATCCTGGAGCAGCGATCGAAATGGGACTCG	572
Db	21	AlaSerSerThrSerAlaSerCylSerAsnProGlyAlaAlaIleGlyAsnGlyAspSer	40
Qy	573	GCGGCGAGCAGAAGTTCTCCGAAGACCCTTAATAGCGAACCTTTCTACTTTGTGCGCG	632
Db	41	AlaAlaSerArgSerSerProLysThrLeuAsnSerGlnProheserThrLeu-Ser--	59
Qy	633	GGTAAGACTTGATGATTTCTCTTTGTCCGAATTATAACACTTCTGTGTTCCAGA	692
Db	60	-----ProAs	61
Qy	693	TCAATTAATAATTGACGCCCAAGAAAGGCACTGAGAAAAGCGACTATCAACTAGTGATTA	752
Db	61	pGlnIleLysLeuThrProGlnGlnGlyThrGlnLysSerGlyLeuSerThrSerAspLys	81
Qy	753	AGCTGCCCACTGGAGGAGCCCAAGGCAAGTGGAATATCTGCCGAGGGAACAACCTATGCT	812
Db	81	SAIaAlaThrGlyAlaProGlySerGlyAsnAsnLeuProGlnGlyGlnThrMetLe	101
Qy	813	AAGCAGAACTCTACGAGACAATCAACTCGTGCCCTAGTCGCTTCTCCACAAACTCCAG	872
Db	101	uArgGlnAsnSerThrSerThrIleAsnSerCylLeuValAlaSerProGlnAsnSerSe	121
Qy	873	TGAACACTCGAATAGCAGCAATGTGTCTGCTACAGTGGGCTTACTCAGATGAGATGG	932
Db	121	rgIuHISerAsnSerSerAsnValSerAlaThrValGlyLeuThrGlnMetValAspCy	141
Qy	933	TGACGAGCAATCGAAGAAAACAAAATGTAGTGTGAAGGACGAGAACTGTGTAAGACTGC	992
Db	141	SAspGlnGlnSerLysLysAsnLysCylSerValLysAspGlnGluAla-----	157
Qy	993	CCTACAATAGTTAAATTTTAAATGTATTTGGCGTTCACTTTGTTAATCATTTAATT	1052
Db	157	-----	157
Qy	1053	GTTTTTTTTTGTCTATACTTACAATTTTAGTTTAACTTGTAACCTTGAACTAAACTCG	1112
Db	157	-----	157
Qy	1113	CGAAGCTCGGATCAAAACAGACATTTTCTTGGAACCGTAATTAAGCTCATTAATAATATTA	1172
Db	157	-----	157

[illegible]

QY 2253 ATAGAAGTCGCTTCACACTCTTGTGGCGGCTTCACCACTACGTGGAGTTCGGCCGCA 2312
Db 226 ----- 226
QY 2313 GNGATTTATATAGATGATTACAGATTATTTAATTTTTATGNGTATTTTAATAATAT 2372
Db 226 ----- 226
QY 2373 CTTATTTATTCATTTTACATAGTTAAATTTGAAAGATTTCAACGACAGTACCACGGA 2432
Db 227 -----Pro-ValIysIleGIuArgIleSerAsnAspSerThrThrGIu 240
QY 2433 AAAAAAGGATCGTCCTTGACAAATGAATATAGCAGAAATGACATGGAAGGTGCAATCAG 2492
Db 241 LysLysGIserSerLeuThrMetAsnAsnAspGIuMetSerMetGIuGIyCysAsnGIu 260
QY 2493 TTGAATCCCGATTTTATCAATGAATCTTAAATATCTGCAATTTGAGCATATTAGTA 2552
Db 261 LeuAsnProAspPheIleAsnGIuSerLeuAsnAsnProAlaIleSerSerIleLeuVal 280
QY 2553 AGCGAGTAGACCAATACCGGGAATCGGAGTTGAGCGGGGACGGAAATTTATGACT 2612
Db 281 SerGIyValGIyProIleProGIyIleGIyValGIyAlaGIyThrGIyAsnLeuLeuThr 300
QY 2613 GCCAAGCCCAATGGAATCTCTCGGGTAGCAGTAATGTTTGGATTACATGCAACAGCA 2672
Db 301 AlaAsnAlaAsnGIyIleSerSerGIySerSerAsnCysLeuAspTyrMetGIuGIuGIu 320
QY 2673 AATCACATATTGCGTGTTCACACTCAGCTGGCCAAACAAAGGGCCGAATCAGTTTAAGC 2732
Db 321 AsnHisIlePheValPheSerThrGIuLeuAlaAsnLysGIyAlaGIuSerValLeuSer 340
QY 2733 GGTCAATTTCAACTATTATGCGTATCAGTCACTGACCTGACTACAAAAGCTTCCTG 2792
Db 341 GIyGIuPheGIuThrIleIleAlaTyrHisCysThrGIuProAlaThrLysSerPheLeu 360
QY 2793 GAAGACTTTTATGA AAAACCTTTAAAGATTAAAGATTAAAGCGGACAAATCCGTC 2852
Db 361 GIuAspPhePheMetLysAsnProLeuLysIleAsnLysLeuGIuAsnArgHisAsnSerVal 380
QY 2853 GGTATGCCATGATAGGCAATGGGGCAGGTTGAGTAATCTCCTCAATCCTGAGCCAA 2912
Db 381 GIyMetProTyrIleGIyMetGIyGIuValGIyLeuThrProProAsnProValAlaLys 400
QY 2913 ATAACACACAGCAGCCACATACAAAGACCGTAGGCTATTGAAACCCCAATTCATCAA 2972
Db 401 IleThrGIuGIuGIuProHisThrLysThrValGIyLeuLeuLysProGIuPheAsnGIu 420
QY 2973 CATGAAAACAGCAAACTAGTACTGTAAAGCGCGCTAGCAACTCTTTGTGACCAAGTCT 3032
Db 421 HisGIuAsnSerLysArgSerThrValSerAlaProSerAsnSerPheValAspGIuSer 440
QY 3033 GATCCTATGGGCAACGAACCTGAATTGATGTGCTGGGAAGCGGATCCTCAACACCAAGT 3092
Db 441 AspProMetGIyAsnGIuThrGIuLeuMetCysTyrGIuGIyGIySerSerAsnThrSer 460
QY 3093 AGGTCTGACAAAACTCACGAATCATGTAGACAGTATCAGTATCCAGGAGTCAAG 3152
Db 461 ArgSerGIyGIuAsnSerArgAsnHisValAspSerIleSerThrSerSerGIuSerGIu 480
QY 3153 GCAATAAAGATACTGGAAGCAGCTGGCGTTGATTGGGACAGGTCACAAAAGGAAGCGAT 3212
Db 481 AlaIleLysIleLeuGIuAlaIaGIyValAspLeuGIyGIuValIThrLysGIySerAsp 500
QY 3213 CCTGGCCTGACAACTGAAAAACAACATTGTATCACTGCAAGAGTTAAGGTTCCAGACGA 3272
Db 501 ProGIyLeuThrThrGIuAsnAsnIleValSerLeuGIuGIyValLysValProAspGIu 520
QY 3273 AACCTTACACACACAGCGGCAACATCGGGAAGAAAGTTGGCAAAAATATAAAAAATG 3332
Db 521 AsnLeuThrProGIuGIuAsnArgIuHisArgGIuGIuGIuLeuAlaLysIleLysLysMet 540

QY 3333 AATCAATTTCTTTTCTGAAAAAGAAATTCAGTAGAGCTAATGTAAAGCTCACAGATA 3392
Db 541 AsnGIuPheLeuPheProGIuAsnGIuAsnSerValGIyAlaAsnValSerSerGIuIle 560
QY 3393 ACAAAAATTCAGAGATTTAATGATGGGATGTGGGTGCGGAGCGGATCTATTATA 3452
Db 561 ThrLysIleProGIyAspLeuMetMetGIyMetSerGIyGIyGIySerIleIle 580
QY 3453 AATCCGAGATGCGACAACTGCATATGCCAGGTAAAGCCCAATCGAGCTCTTATCGGCG 3512
Db 581 AsnProThrMetArgGIuLeuHisMetProGIyAsnAlaLysSerGIuLeuLeuSerAla 600
QY 3513 ACAAGTTCAGAGCTTTCCGAAGATGTATGATCATCCAGGGGATGTTATATCAGATATGGT 3572
Db 601 ThrSerSerGIyLeuSerGIuAspValMetHisProGIyAspValIleSerAspMetGIy 620
QY 3573 GCCGTATAGGATGTATTAATATCAAAAAACAGTGTGCAATGTGGATCTGAGTAGGT 3632
Db 621 AlaValIleGIyCysAsnAsnAsnGIuLysThrSerValGIuCysGIySerGIyValGIy 640
QY 3633 GTTGCTACTGGAACAACTGCAGCTGGAGTAAATGTCAATATGCAATTGCTCAAGCTCCGGC 3692
Db 641 ValValThrGIyThrThrAlaAlaGIyValAsnValAsnMetHisCysSerSerSerGIy 660
QY 3693 GCCCGGAATGGCAATGTATGAGGGAAGCTCTACGGAATATGCTAGCCTCGTTGGCAACACA 3752
Db 661 AlaProAsnGIyAsnMetMetGIySerSerThrAspMetLeuAlaSerPheGIyAsnThr 680
QY 3753 AGCTGCAACGTCAATCGGAACGGCCCCAGATATGTCTTAAGGAAGTTTAAATCAAGATAGC 3812
Db 681 SerCysAsnValIleGIyThrAlaProAspMetSerLysGIuValLeuAsnGIuAspSer 700
QY 3813 CGAACCATTCAATCAAGGGGAGTTGCTCAATGGAAGTGTGGAAGATTCAACATCAA 3872
Db 701 ArgThrHisSerHisGIuGIyGIyValAlaGIuMetGIuTyrSerLysIleGIuHisGIu 720
QY 3873 TTTTTCGAAGAACGCTCAAGGGGGGCAAGCCCAAGCAAGTCACTGGAAGTGTAGTACA 3932
Db 721 PhePheGIuGIuArgLeuLysGIyGIyLysProArgGIuValIThrGIyThrValValPro 740
QY 3933 CAACAGCAAAACCCCTTCTGATCTGTGGAACCTCGTTAAACAACAGGTGCAACCCCTG 3992
Db 741 GIuGIuGIuGIuThrProSerGIySerGIyGIyAsnSerLeuAsnAsnGIuValArgProLeu 760
QY 3993 CAAGTCCACCTCCTTACCACTCCATCCAGAGATCTGCGTCACTACCAATAGCACT 4052
Db 761 GIuGIyProProProProTyrHisSerIleGIuAsnSerAlaSerValProIleAlaThr 780
QY 4053 CAATGCCCAATCCCTCGAGTCCAAACAATCTATCTCTCCGTCACCCGCGACAAACCGCA 4112
Db 781 GIuSerProAsnProSerSerProAsnAsnLeuSerLeuProSerProArgThrThrAla 800
QY 4113 GCAGTCATGGGATTGCCGACCAACTCTCTAGCATGATGGAACAGAGCATTAATCTGGA 4172
Db 801 AlaValMetGIyLeuProThrAsnSerProSerMetAspGIyThrGIySerLeuSerGIy 820
QY 4173 TCTGTTCCGCAAGCTAATACTTGCAGCGTTCAAGGACGACCAACAACAGTGTCTCAGCA 4232
Db 821 SerValProGIuAlaAsnThrSerThrValGIuAlaGIyThrThrThrValLeuSerAla 840
QY 4233 AACCAAGACTGTTTCAAGGACAGACACCCCATCGCGTCAAAATCAAAATCGTAGAAT 4292
Db 841 AsnLysAsnCysPheGIuAlaAspThrProSerProSerAsnGIuAsnArgSerArgAsn 860
QY 4293 ACCGATCGTCAAGCGTCTTACGCAATACTTAAGCAGCAACCCCAAGTACCCCTTATCT 4352
Db 861 ThrGIySerSerSerValLeuThrHisAsnLeuSerSerAsnProSerThrProLeuSer 880
QY 4353 CATCTATCCCAAGGAATTTGAGTCTTTCGGTCAGTCTCTGCTGTAATGTATATTG 4412
Db 881 HisLeuSerProLysGIuPheGIuSerPheGIyGIuInSerSer----- 894
QY 4413 TTTAATTTTTTAAAGCAAAATCAATATGAATTGCGTTAATAATTAATTATATTA 4472

where are the
5482-5601
enc aa 1140-1179?

Db 894 ----- 894
QY 4473 TAACTCGAAATTGATAGAAAAATCAGGAATAGAAAAATAATTATTTCCGACCG 4532
Db 894 ----- 894
QY 4533 CCCATCCATTCTGAAATCCAAATTTCTGAGTGATGTTAGAGATAATCTACTATTAAAA 4592
Db 894 ----- 894
QY 4593 TTAAACACGAAATTCATATCCGTTAATTGAAAATCACTATTGTTAATAGAAATTAAA 4652
Db 894 ----- 894
QY 4653 AATATGTTATTATTAATATTTCTACAGGTGATTAACATGAAAAAGTAGCGCAAGCCAC 4712
Db 895 -----Ala--GlyAspAsnMetLysSerArgArgProSerProG 907
QY 4713 AGGTCAGCGGTACAGCAATAATAGTCTAATAGAGCAATAAAGATGTACGATTGCTG 4772
Db 907 lnglYglNargSerProValAsnSerLeuileGluAlaAsnLysAspValArgPheAla 927
QY 4773 CATCCAGTCTGTTTAAACCCGCATCCACATATGCAAGCAATTCAATTCAGCATTA 4832
Db 927 laSerSerProGlyPheAsnProHisProHisMetGlnSerAsnSerAlaLeuA 947
QY 4833 AGCCTATAAAATGGGCTCTACCAATATACAGATGAGGTAAATATTAAATATTTATT 4892
Db 947 snAlaTyrlYsMetGlySerThrAsnileGlnMetGlu--Arg----- 960
QY 4893 TAAAGTTTGTGTTAATTATCTTTTTCAGCGTCAGCATCAGCGCAAGGTGATC 4952
Db 961 -----GlnAlaSerAlaGlnGlySe 968
QY 4953 CGTACAATTAGTCGGCGCTCCGATATATTCGCTAAATCCCAATAGTGGCAATCGGC 5012
Db 968 rValGlnPheSerArgSerAspAsnileProLeuAsnProAsnSerGlyAsnArgPr 988
QY 5013 GCCACCAAAACAAGATGACCCAAAACCTTCGATCCAAATCTTCTTGGCACAATGCCA 5072
Db 988 oProProAsnLysMetThrGlnAsnPheAspProIleSerSerLeuAlaGlnMetSerG 1008
QY 5073 ACACTAACAAGTTCGCTGTCAGCATGGGTAGTCCAGCCGGAAGTGGTATGACAT 5132
Db 1008 nGlnLeuThrSerCysValSerSerMetGlySerProAlaGlyThrGlyMetThrMe 1028
QY 5133 GATGGGGGGTCCGGGACCGTCCGACATCAATATTTAGCATGGAATATTCGGGACTGA 5192
Db 1028 tMetGlyGlyProGlyProSerAspIleAsnileGlnHisGlyIleIleSerGlyLeuAs 1048
QY 5193 TGGATCAGGAATAGATACATAAATCAAAATACCTGTCATTCATGAATGTCGTAATGA 5252
Db 1048 pGlySerGlyIleAspThrIleAsnGlnAsnAsnCyHisSerMetAsnValValMetAs 1068
QY 5253 CTCAATGGTCCCGAATGCTGAATCTTAAATGTGCTAGCAGCGGTCCAAATGGACC 5312
Db 1068 nSerMetGlyProArgMetLeuAsnProLysMetCysValAlaGlyGlyProAsnGlyPr 1088
QY 5313 GCCTGCTTTAATCTTAATCCCCCAATGCTGATTAAGAGAAATTCATAGGGTCTGG 5372
Db 1088 oProGlyPheAsnProAsnSerProAsnGlyGlyLeuArgGlyAsnSerIleGlySerG 1108
QY 5373 CTGTGGCTCAGCAAACTCTTCAAACTTCAAGGGGTTTCCACCTGGTCCAGATGAT 5432
Db 1108 yCySglYserAlaAsnSerSerAsnPheGlnGlyValProProGlyAlaArgMetMe 1128
QY 5433 GGGTCGAATGCCAGTCAATTTGTTGGAATTCATCCGAATATTCAGGTAAGGCGAG 5492
Db 1128 tGlyArgMetProValAsnPheGlySerAsnPheAsnProAsnile----- 1143
QY 5493 TACCCCAAAACCATATACATATGCTCAGTAAGGGCAGAAAGCCCAACAATTAACA 5552

Db 1143 ----- 1143
QY 5553 CAATGAGCTAATATGTGCGAATGCCACTAGTCTGAATTTTGCAGAGTACGCTAA 5612
Db 1144 -----GlnArgTyrlAlaAs 1148
QY 5613 CCCTCAATGGTGTCTGTAGGCAATGGGTGCCAATATGCCCCACCATCAGCCAGCGAG 5672
Db 1148 nProGlnMetGlyAlaValAlaGlyAsnGlySerProIleCysProProSerAlaSerAspG 1168
QY 5673 TACTCCTGAATGCCAGATTGATGGCGGACAGAGCCGAGGTATGCTAATGAATTC 5732
Db 1168 yThrProGlyMetProGlyLeuMetAlaGlyProGlyAlaGlyGlyMetLeuMetAsnSe 1188
QY 5733 TTCCGAGAGACAACAGAACAGATCAACAATCCTGGGCGCAAGCAATGCTATTAA 5792
Db 1188 rSerGlyGlnGlnHisGlnAsnLysIleThrAsnAsnProGlyAlaSerAsnGlyIleAs 1208
QY 5793 CTTCTTCAAGATTGCAATCAATGTCTATTGTTGACGAAGAGGTGATTACCCGGCCA 5852
Db 1208 nPhePheGlnAsnCyAsnGlnMetSerIleValAspGlnGlnGlyGlyLeuProGlyHi 1228
QY 5853 TGACGGAATCAATGAATATTGTCACCAATCTATGATTAAGGGGATGCGTCCACATGCCAT 5912
Db 1228 sAspGlySerMetAsnileGlyGlnProSerMetIleArgGlyMetArgProHisAlaMe 1248
QY 5913 GCGGCCAAATGTAATGGGTGCGCGGATGCCACCGTTAACAGGCAATTCAGTTTGACA 5972
Db 1248 tArgProAsnValMetGlyAlaArgMetProProValAsnArgGlnileGlnPheAlaG 1268
QY 5973 GTCATCGAATGATATGACTGTGTGCGGGATCCGTATCATTTTTCATTAACGCTTCCTG 6032
Db 1268 nSerSerAspGlyIleAspCysValGlyAspProSerSerPhePheThrAsnAlaSerCy 1288
QY 6033 CAACAGCGTGAACACACATGTTTGGATGACACAACAGGCGCAATCAGCCTAAGACACA 6092
Db 1288 sAsnSerAlaGlyProHisMetPheGlySerAlaGlnGlnAlaAsnGlnProLysThrG 1308
QY 6093 ACACATAAAGACATACCTAGTGAATGTTCAAAACCAATCGGGAATTCGAGTGGCACA 6152
Db 1308 nHisIleLysAsnIleProSerGlyMetCysGlnAsnGlnSerGlyLeuAlaValAlaG 1328
QY 6153 AGGCGAGATCCAATGTCATGGGCAAGACATGCGCAGGTCAGTCTTTAATTGACCTAC 6212
Db 1328 nGlyGlnIleGlnLeuHisGlyGlnGlyHisAlaGlnGlnGlnSerLeuileGlyProTh 1348
QY 6213 TAATAATAATTATGTCAACTGCCGAAGTGTCAAGTGTACTTAACGGTGTCTGSCAT 6272
Db 1348 rAsnAsnAsnLeuMetSerThrAlaGlySerValSerAlaThrAsnGlyValSerGlyI 1368
QY 6273 CAATTGCTAGTCCCTCTTCTACGAGCTGAAGTATGCCAGCAATATGATGTTTCA 6332
Db 1368 eAsnPheValGlyProSerSerThrAspLeuLysTyrlAlaGlnGlnTyHisSerPheG 1388
QY 6333 GCAGCAGTTATGCTACCAACACAGAGTCAACAACAACAGCATATGCAAGCAGACA 6392
Db 1388 nGlnGlnLeuTyrlaThrAsnThrArgSerGlnGlnGlnHisIleMetHisGlnGlnHi 1408
QY 6393 CCAAGACAATGATTAACAATGCGCGCGAATTTATCAACCAATCCAAGTCTTTGTCAA 6452
Db 1408 sGlnSerAsnMetIleThrMetProProAsnLeuSerProAsnProThrPhePheValAs 1428
QY 6453 CAAA 6456
Db 1428 nLys 1429

RESULT 2
US-09-915-543-10
; Sequence 10, Application US/09915543
; Publication No. US20020086986A1
; GENERAL INFORMATION:
; APPLICANT: BASLER, Konrad
; APPLICANT: BRUNNER, Brich

Attach #3



United States Patent and Trademark Office

[Home](#) | [Site Index](#) | [Search](#) | [FAQ](#) | [Glossary](#) | [Guides](#) | [Contacts](#) | [eBusiness](#) | [eBiz alerts](#) | [News](#) | [Help](#)

Publication Site for Issued and Published Sequences (PSIPS)

PSIPS View Sequence(s): 3129 for 20050208558

PSIPS Homepage

Here is the list of the requested sequences.

Sequence ID

No:

Go

First
SequenceNext
SequencePrevious
SequenceLast
SequenceFull Text
PublicationPSIPS Home
PageNCBI Home
PIW and AIW
Search Home
PageDocument
ServicesDivision
USPTO HomeHelp Page
FAQConvi
to
Searc
Form:

<210> SEQ ID NO 3129

<211> LENGTH: 1429

<212> TYPE: PRT

<213> ORGANISM: DROSOPHILA

<400> SEQUENCE: 3129

Basler et al →

Met	Leu	Ser	Thr	Thr	Met	Pro	Arg	Ser	Pro	Thr	Gln	Gln	Gln	Pro	Gln
1				5					10					15	
Pro	Asn	Ser	Asp	Ala	Ser	Ser	Thr	Ser	Ala	Ser	Gly	Ser	Asn	Pro	Gly
			20					25					30		
Ala	Ala	Ile	Gly	Asn	Gly	Asp	Ser	Ala	Ala	Ser	Arg	Ser	Ser	Pro	Lys
		35				40					45				
Thr	Leu	Asn	Ser	Glu	Pro	Phe	Ser	Thr	Leu	Ser	Pro	Asp	Gln	Ile	Lys
	50					55					60				
Leu	Thr	Pro	Glu	Glu	Gly	Thr	Glu	Lys	Ser	Gly	Leu	Ser	Thr	Ser	Asp
65					70					75					80
Lys	Ala	Ala	Thr	Gly	Gly	Ala	Pro	Gly	Ser	Gly	Asn	Asn	Leu	Pro	Glu
				85					90					95	
Gly	Gln	Thr	Met	Leu	Arg	Gln	Asn	Ser	Thr	Ser	Thr	Ile	Asn	Ser	Cys
			100					105					110		
Leu	Val	Ala	Ser	Pro	Gln	Asn	Ser	Ser	Glu	His	Ser	Asn	Ser	Ser	Asn
		115					120					125			
Val	Ser	Ala	Thr	Val	Gly	Leu	Thr	Gln	Met	Val	Asp	Cys	Asp	Glu	Gln
	130					135					140				
Ser	Lys	Lys	Asn	Lys	Cys	Ser	Val	Lys	Asp	Glu	Glu	Ala	Glu	Ile	Ser
145					150					155					160
Ser	Asn	Lys	Ala	Lys	Gly	Gln	Ala	Ala	Gly	Gly	Gly	Cys	Glu	Thr	Gly
			165						170					175	
Ser	Thr	Ser	Ser	Leu	Thr	Val	Lys	Glu	Glu	Pro	Thr	Asp	Val	Leu	Gly
			180					185					190		
Ser	Leu	Val	Asn	Met	Lys	Lys	Glu	Glu	Arg	Glu	Asn	His	Ser	Pro	Thr
		195					200					205			
Met	Ser	Pro	Val	Gly	Phe	Gly	Ser	Ile	Gly	Asn	Ala	Gln	Asp	Asn	Ser
	210					215					220				
Ala	Thr	Pro	Val	Lys	Ile	Glu	Arg	Ile	Ser	Asn	Asp	Ser	Thr	Thr	Glu
225					230					235					240
Lys	Lys	Gly	Ser	Ser	Leu	Thr	Met	Asn	Asn	Asp	Glu	Met	Ser	Met	Glu
			245						250				255		
Gly	Cys	Asn	Gln	Leu	Asn	Pro	Asp	Phe	Ile	Asn	Glu	Ser	Leu	Asn	Asn
		260						265					270		
Pro	Ala	Ile	Ser	Ser	Ile	Leu	Val	Ser	Gly	Val	Gly	Pro	Ile	Pro	Gly
		275					280					285			
Ile	Gly	Val	Gly	Ala	Gly	Thr	Gly	Asn	Leu	Leu	Thr	Ala	Asn	Ala	Asn
	290					295					300				
Gly	Ile	Ser	Ser	Gly	Ser	Ser	Asn	Cys	Leu	Asp	Tyr	Met	Gln	Gln	Gln
305						310				315					320
Asn	His	Ile	Phe	Val	Phe	Ser	Thr	Gln	Leu	Ala	Asn	Lys	Gly	Ala	Glu
			325						330				335		
Ser	Val	Leu	Ser	Gly	Gln	Phe	Gln	Thr	Ile	Ile	Ala	Tyr	His	Cys	Thr

				340				345					350				
Gln	Pro	Ala	Thr	Lys	Ser	Phe	Leu	Glu	Asp	Phe	Phe	Met	Lys	Asn	Pro		
		355					360					365					
Leu	Lys	Ile	Asn	Lys	Leu	Gln	Arg	His	Asn	Ser	Val	Gly	Met	Pro	Trp		
	370					375					380						
Ile	Gly	Met	Gly	Gln	Val	Gly	Leu	Thr	Pro	Pro	Asn	Pro	Val	Ala	Lys		
385					390					395					400		
Ile	Thr	Gln	Gln	Gln	Pro	His	Thr	Lys	Thr	Val	Gly	Leu	Leu	Lys	Pro		
				405					410					415			
Gln	Phe	Asn	Gln	His	Glu	Asn	Ser	Lys	Arg	Ser	Thr	Val	Ser	Ala	Pro		
		420						425				430					
Ser	Asn	Ser	Phe	Val	Asp	Gln	Ser	Asp	Pro	Met	Gly	Asn	Glu	Thr	Glu		
	435						440				445						
Leu	Met	Cys	Trp	Glu	Gly	Gly	Ser	Ser	Asn	Thr	Ser	Arg	Ser	Gly	Gln		
	450				455					460							
Asn	Ser	Arg	Asn	His	Val	Asp	Ser	Ile	Ser	Thr	Ser	Ser	Glu	Ser	Gln		
465				470						475					480		
Ala	Ile	Lys	Ile	Leu	Glu	Ala	Ala	Gly	Val	Asp	Leu	Gly	Gln	Val	Thr		
			485					490					495				
Lys	Gly	Ser	Asp	Pro	Gly	Leu	Thr	Thr	Glu	Asn	Asn	Ile	Val	Ser	Leu		
		500						505				510					
Gln	Gly	Val	Lys	Val	Pro	Asp	Glu	Asn	Leu	Thr	Pro	Gln	Gln	Arg	Gln		
	515						520					525					
His	Arg	Glu	Glu	Gln	Leu	Ala	Lys	Ile	Lys	Lys	Met	Asn	Gln	Phe	Leu		
	530					535					540						
Phe	Pro	Glu	Asn	Glu	Asn	Ser	Val	Gly	Ala	Asn	Val	Ser	Ser	Gln	Ile		
545				550						555					560		
Thr	Lys	Ile	Pro	Gly	Asp	Leu	Met	Met	Gly	Met	Ser	Gly	Gly	Gly	Gly		
			565					570						575			
Gly	Ser	Ile	Ile	Asn	Pro	Thr	Met	Arg	Gln	Leu	His	Met	Pro	Gly	Asn		
		580						585					590				
Ala	Lys	Ser	Glu	Leu	Leu	Ser	Ala	Thr	Ser	Ser	Gly	Leu	Ser	Glu	Asp		
	595						600					605					
Val	Met	His	Pro	Gly	Asp	Val	Ile	Ser	Asp	Met	Gly	Ala	Val	Ile	Gly		
	610					615					620						
Cys	Asn	Asn	Asn	Gln	Lys	Thr	Ser	Val	Gln	Cys	Gly	Ser	Gly	Val	Gly		
625				630						635					640		
Val	Val	Thr	Gly	Thr	Thr	Ala	Ala	Gly	Val	Asn	Val	Asn	Met	His	Cys		
			645					650						655			
Ser	Ser	Ser	Gly	Ala	Pro	Asn	Gly	Asn	Met	Met	Gly	Ser	Ser	Thr	Asp		
		660						665						670			
Met	Leu	Ala	Ser	Phe	Gly	Asn	Thr	Ser	Cys	Asn	Val	Ile	Gly	Thr	Ala		
	675						680					685					
Pro	Asp	Met	Ser	Lys	Glu	Val	Leu	Asn	Gln	Asp	Ser	Arg	Thr	His	Ser		
	690									700							
His	Gln	Gly	Gly	Val	Ala	Gln	Met	Glu	Trp	Ser	Lys	Ile	Gln	His	Gln		
705				710						715					720		
Phe	Phe	Glu	Glu	Arg	Leu	Lys	Gly	Gly	Lys	Pro	Arg	Gln	Val	Thr	Gly		
			725					730						735			
Thr	Val	Val	Pro	Gln	Gln	Gln	Thr	Pro	Ser	Gly	Ser	Gly	Gly	Asn	Ser		
		740						745				750					
Leu	Asn	Asn	Gln	Val	Arg	Pro	Leu	Gln	Gly	Pro	Pro	Pro	Pro	Tyr	His		
	755						760					765					
Ser	Ile	Gln	Arg	Ser	Ala	Ser	Val	Pro	Ile	Ala	Thr	Gln	Ser	Pro	Asn		
	770					775					780						
Pro	Ser	Ser	Pro	Asn	Asn	Leu	Ser	Leu	Pro	Ser	Pro	Arg	Thr	Thr	Ala		
785				790						795					800		
Ala	Val	Met	Gly	Leu	Pro	Thr	Asn	Ser	Pro	Ser	Met	Asp	Gly	Thr	Gly		
			805					810						815			
Ser	Leu	Ser	Gly	Ser	Val	Pro	Gln	Ala	Asn	Thr	Ser	Thr	Val	Gln	Ala		
			820					825					830				
Gly	Thr	Thr	Thr	Val	Leu	Ser	Ala	Asn	Lys	Asn	Cys	Phe	Gln	Ala	Asp		

insert
1140 - 1179
Bosler

1330	1335	1340
Ile Gly Pro Thr Asn Asn Asn Leu Met Ser Thr Ala Gly Ser Val Ser		
1345	1350	1355
Ala Thr Asn Gly Val Ser Gly Ile Asn Phe Val Gly Pro Ser Ser Thr		1360
	1365	1370
Asp Leu Lys Tyr Ala Gln Gln Tyr His Ser Phe Gln Gln Gln Leu Tyr		1375
	1380	1385
Ala Thr Asn Thr Arg Ser Gln Gln Gln Gln His Met His Gln Gln His		1390
	1395	1400
Gln Ser Asn Met Ile Thr Met Pro Pro Asn Leu Ser Pro Asn Pro Thr		1405
	1410	1415
Phe Phe Val Asn Lys		1420
1425		

1464

[PSIPS Home](#) | [PSIPS Help Page](#) | [PSIPS Accessibility Help Page](#) | [PSIPS FAQ](#) |
[PIW and AIW Search Home Page](#) | [Document Services Division](#) |
[NCBI Home](#)

[HOME](#) | [INDEX](#) | [SEARCH](#) | [eBUSINESS](#) | [CONTACT US](#) | [PRIVACY STATEMENT](#)

Last Modified: 11/15/2005 14:31:29